

Early Registration Fee
\$475 + tax

Late Registration Fee
is an additional \$200

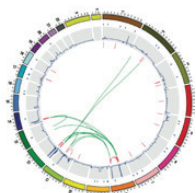
Limited to 30 participants
per workshop



Canadian Bioinformatics Workshop Series

Awards available for CBW workshops

Informatics on High-throughput Sequencing Data



Dates

June 9-10, 2016 - Montreal, Quebec

Faculty

Guillaume Bourque, Francis Ouellette and Jared Simpson

Course Objectives

With the introduction of high-throughput sequencing platforms it is becoming feasible to consider sequencing approaches to address many research projects. However, knowing how to manage and interpret the large volume of sequence data resulting from such technologies is less clear. The CBW offers a **two-day workshop** covering the bioinformatics tools available for managing and interpreting high-throughput sequencing data from Illumina reads using a reference genome. We will also cover the theory of *de novo* genome assembly, common steps that assemblers perform and provide an overview of commonly used software.

Beginning with an understanding of the workflow involved to move from platform images to sequence generation, participants will gain practical experience and skills to be able to:

- Assess sequence quality;
- Map sequence data onto a reference genome (required);
- Visualize and interrogate sequence data;
- Integrate biological context with sequence information.

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For information send an email to:
course_info@bioinformatics.ca

For course requirements and to apply
visit: bioinformatics.ca